













26-NOV-1999; 99BK-0001691.  
 PK 07-FEB-2000; 2000BK-0000194.  
 PK 07-MAR-2000; 2000BK-0000463.  
 PK 14-APR-2000; 2000BK-0000642.  
 XX  
 PA (MAXY-) MAXYGEN APS.  
 XX  
 P1 Pedersen AH, Schambly HT, Anderson KV, Bornaes C, Rasmussen PR.  
 WP1: 2001.218488/22.  
 XX  
 DNR A conjugate exhibiting interferon beta activity useful for treating  
 P1 multiple sclerosis comprises a non-polypeptide group covalently  
 P2 attached to an interferon beta polypeptide.  
 P3  
 P4  
 P5  
 P6  
 P7  
 P8  
 P9  
 P10  
 P11  
 P12  
 P13  
 P14  
 P15  
 P16  
 P17  
 P18  
 P19  
 P20  
 P21  
 P22  
 P23  
 P24  
 P25  
 P26  
 P27  
 P28  
 P29  
 P30  
 P31  
 P32  
 P33  
 P34  
 P35  
 P36  
 P37  
 P38  
 P39  
 P40  
 P41  
 P42  
 P43  
 P44  
 P45  
 P46  
 P47  
 P48  
 P49  
 P50  
 P51  
 P52  
 P53  
 P54  
 P55  
 P56  
 P57  
 P58  
 P59  
 P60  
 P61  
 P62  
 P63  
 P64  
 P65  
 P66  
 P67  
 P68  
 P69  
 P70  
 P71  
 P72  
 P73  
 P74  
 P75  
 P76  
 P77  
 P78  
 P79  
 P80  
 P81  
 P82  
 P83  
 P84  
 P85  
 P86  
 P87  
 P88  
 P89  
 P90  
 P91  
 P92  
 P93  
 P94  
 P95  
 P96  
 P97  
 P98  
 P99  
 P100  
 P101  
 P102  
 P103  
 P104  
 P105  
 P106  
 P107  
 P108  
 P109  
 P110  
 P111  
 P112  
 P113  
 P114  
 P115  
 P116  
 P117  
 P118  
 P119  
 P120  
 P121  
 P122  
 P123  
 P124  
 P125  
 P126  
 P127  
 P128  
 P129  
 P130  
 P131  
 P132  
 P133  
 P134  
 P135  
 P136  
 P137  
 P138  
 P139  
 P140  
 P141  
 P142  
 P143  
 P144  
 P145  
 P146  
 P147  
 P148  
 P149  
 P150  
 P151  
 P152  
 P153  
 P154  
 P155  
 P156  
 P157  
 P158  
 P159  
 P160  
 P161  
 P162  
 P163  
 P164  
 P165  
 P166  
 P167  
 P168  
 P169  
 P170  
 P171  
 P172  
 P173  
 P174  
 P175  
 P176  
 P177  
 P178  
 P179  
 P180  
 P181  
 P182  
 P183  
 P184  
 P185  
 P186  
 P187  
 P188  
 P189  
 P190  
 P191  
 P192  
 P193  
 P194  
 P195  
 P196  
 P197  
 P198  
 P199  
 P200  
 P201  
 P202  
 P203  
 P204  
 P205  
 P206  
 P207  
 P208  
 P209  
 P210  
 P211  
 P212  
 P213  
 P214  
 P215  
 P216  
 P217  
 P218  
 P219  
 P220  
 P221  
 P222  
 P223  
 P224  
 P225  
 P226  
 P227  
 P228  
 P229  
 P230  
 P231  
 P232  
 P233  
 P234  
 P235  
 P236  
 P237  
 P238  
 P239  
 P240  
 P241  
 P242  
 P243  
 P244  
 P245  
 P246  
 P247  
 P248  
 P249  
 P250  
 P251  
 P252  
 P253  
 P254  
 P255  
 P256  
 P257  
 P258  
 P259  
 P260  
 P261  
 P262  
 P263  
 P264  
 P265  
 P266  
 P267  
 P268  
 P269  
 P270  
 P271  
 P272  
 P273  
 P274  
 P275  
 P276  
 P277  
 P278  
 P279  
 P280  
 P281  
 P282  
 P283  
 P284  
 P285  
 P286  
 P287  
 P288  
 P289  
 P290  
 P291  
 P292  
 P293  
 P294  
 P295  
 P296  
 P297  
 P298  
 P299  
 P300  
 P301  
 P302  
 P303  
 P304  
 P305  
 P306  
 P307  
 P308  
 P309  
 P310  
 P311  
 P312  
 P313  
 P314  
 P315  
 P316  
 P317  
 P318  
 P319  
 P320  
 P321  
 P322  
 P323  
 P324  
 P325  
 P326  
 P327  
 P328  
 P329  
 P330  
 P331  
 P332  
 P333  
 P334  
 P335  
 P336  
 P337  
 P338  
 P339  
 P340  
 P341  
 P342  
 P343  
 P344  
 P345  
 P346  
 P347  
 P348  
 P349  
 P350  
 P351  
 P352  
 P353  
 P354  
 P355  
 P356  
 P357  
 P358  
 P359  
 P360  
 P361  
 P362  
 P363  
 P364  
 P365  
 P366  
 P367  
 P368  
 P369  
 P370  
 P371  
 P372  
 P373  
 P374  
 P375  
 P376  
 P377  
 P378  
 P379  
 P380  
 P381  
 P382  
 P383  
 P384  
 P385  
 P386  
 P387  
 P388  
 P389  
 P390  
 P391  
 P392  
 P393  
 P394  
 P395  
 P396  
 P397  
 P398  
 P399  
 P400  
 P401  
 P402  
 P403  
 P404  
 P405  
 P406  
 P407  
 P408  
 P409  
 P410  
 P411  
 P412  
 P413  
 P414  
 P415  
 P416  
 P417  
 P418  
 P419  
 P420  
 P421  
 P422  
 P423  
 P424  
 P425  
 P426  
 P427  
 P428  
 P429  
 P430  
 P431  
 P432  
 P433  
 P434  
 P435  
 P436  
 P437  
 P438  
 P439  
 P440  
 P441  
 P442  
 P443  
 P444  
 P445  
 P446  
 P447  
 P448  
 P449  
 P450  
 P451  
 P452  
 P453  
 P454  
 P455  
 P456  
 P457  
 P458  
 P459  
 P460  
 P461  
 P462  
 P463  
 P464  
 P465  
 P466  
 P467  
 P468  
 P469  
 P470  
 P471  
 P472  
 P473  
 P474  
 P475  
 P476  
 P477  
 P478  
 P479  
 P480  
 P481  
 P482  
 P483  
 P484  
 P485  
 P486  
 P487  
 P488  
 P489  
 P490  
 P491  
 P492  
 P493  
 P494  
 P495  
 P496  
 P497  
 P498  
 P499  
 P500  
 P501  
 P502  
 P503  
 P504  
 P505  
 P506  
 P507  
 P508  
 P509  
 P510  
 P511  
 P512  
 P513  
 P514  
 P515  
 P516  
 P517  
 P518  
 P519  
 P520  
 P521  
 P522  
 P523  
 P524  
 P525  
 P526  
 P527  
 P528  
 P529  
 P530  
 P531  
 P532  
 P533  
 P534  
 P535  
 P536  
 P537  
 P538  
 P539  
 P540  
 P541  
 P542  
 P543  
 P544  
 P545  
 P546  
 P547  
 P548  
 P549  
 P550  
 P551  
 P552  
 P553  
 P554  
 P555  
 P556  
 P557  
 P558  
 P559  
 P560  
 P561  
 P562  
 P563  
 P564  
 P565  
 P566  
 P567  
 P568  
 P569  
 P570  
 P571  
 P572  
 P573  
 P574  
 P575  
 P576  
 P577  
 P578  
 P579  
 P580  
 P581  
 P582  
 P583  
 P584  
 P585  
 P586  
 P587  
 P588  
 P589  
 P590  
 P591  
 P592  
 P593  
 P594  
 P595  
 P596  
 P597  
 P598  
 P599  
 P600  
 P601  
 P602  
 P603  
 P604  
 P605  
 P606  
 P607  
 P608  
 P609  
 P610  
 P611  
 P612  
 P613  
 P614  
 P615  
 P616  
 P617  
 P618  
 P619  
 P620  
 P621  
 P622  
 P623  
 P624  
 P625  
 P626  
 P627  
 P628  
 P629  
 P630  
 P631  
 P632  
 P633  
 P634  
 P635  
 P636  
 P637  
 P638  
 P639  
 P640  
 P641  
 P642  
 P643  
 P644  
 P645  
 P646  
 P647  
 P648  
 P649  
 P650  
 P651  
 P652  
 P653  
 P654  
 P655  
 P656  
 P657  
 P658  
 P659  
 P660  
 P661  
 P662  
 P663  
 P664  
 P665  
 P666  
 P667  
 P668  
 P669  
 P670  
 P671  
 P672  
 P673  
 P674  
 P675  
 P676  
 P677  
 P678  
 P679  
 P680  
 P681  
 P682  
 P683  
 P684  
 P685  
 P686  
 P687  
 P688  
 P689  
 P690  
 P691  
 P692  
 P693  
 P694  
 P695  
 P696  
 P697  
 P698  
 P699  
 P700  
 P701  
 P702  
 P703  
 P704  
 P705  
 P706  
 P707  
 P708  
 P709  
 P710  
 P711  
 P712  
 P713  
 P714  
 P715  
 P716  
 P717  
 P718  
 P719  
 P720  
 P721  
 P722  
 P723  
 P724  
 P725  
 P726  
 P727  
 P728  
 P729  
 P730  
 P731  
 P732  
 P733  
 P734  
 P735  
 P736  
 P737  
 P738  
 P739  
 P740  
 P741  
 P742  
 P743  
 P744  
 P745  
 P746  
 P747  
 P748  
 P749  
 P750  
 P751  
 P752  
 P753  
 P754  
 P755  
 P756  
 P757  
 P758  
 P759  
 P760  
 P761  
 P762  
 P763  
 P764  
 P765  
 P766  
 P767  
 P768  
 P769  
 P770  
 P771  
 P772  
 P773  
 P774  
 P775  
 P776  
 P777  
 P778  
 P779  
 P780  
 P781  
 P782  
 P783  
 P784  
 P785  
 P786  
 P787  
 P788  
 P789  
 P790  
 P791  
 P792  
 P793  
 P794  
 P795  
 P796  
 P797  
 P798  
 P799  
 P800  
 P801  
 P802  
 P803  
 P804  
 P805  
 P806  
 P807  
 P808  
 P809  
 P810  
 P811  
 P812  
 P813  
 P814  
 P815  
 P816  
 P817  
 P818  
 P819  
 P820  
 P821  
 P822  
 P823  
 P824  
 P825  
 P826  
 P827  
 P828  
 P829  
 P830  
 P831  
 P832  
 P833  
 P834  
 P835  
 P836  
 P837  
 P838  
 P839  
 P840  
 P841  
 P842  
 P843  
 P844  
 P845  
 P846  
 P847  
 P848  
 P849  
 P850  
 P851  
 P852  
 P853  
 P854  
 P855  
 P856  
 P857  
 P858  
 P859  
 P860  
 P861  
 P862  
 P863  
 P864  
 P865  
 P866  
 P867  
 P868  
 P869  
 P870  
 P871  
 P872  
 P873  
 P874  
 P875  
 P876  
 P877  
 P878  
 P879  
 P880  
 P881  
 P882  
 P883  
 P884  
 P885  
 P886  
 P887  
 P888  
 P889  
 P890  
 P891  
 P892  
 P893  
 P894  
 P895  
 P896  
 P897  
 P898  
 P899  
 P900  
 P901  
 P902  
 P903  
 P904  
 P905  
 P906  
 P907  
 P908  
 P909  
 P910  
 P911  
 P912  
 P913  
 P914  
 P915  
 P916  
 P917  
 P918  
 P919  
 P920  
 P921  
 P922  
 P923  
 P924  
 P925  
 P926  
 P927  
 P928  
 P929  
 P930  
 P931  
 P932  
 P933  
 P934  
 P935  
 P936  
 P937  
 P938  
 P939  
 P940  
 P941  
 P942  
 P943  
 P944  
 P945  
 P946  
 P947  
 P948  
 P949  
 P950  
 P951  
 P952  
 P953  
 P954  
 P955  
 P956  
 P957  
 P958  
 P959  
 P960  
 P961  
 P962  
 P963  
 P964  
 P965  
 P966  
 P967  
 P968  
 P969  
 P970  
 P971  
 P972  
 P973  
 P974  
 P975  
 P976  
 P977  
 P978  
 P979  
 P980  
 P981  
 P982  
 P983  
 P984  
 P985  
 P986  
 P987  
 P988  
 P989  
 P990  
 P991  
 P992  
 P993  
 P994  
 P995  
 P996  
 P997  
 P998  
 P999  
 P1000  
 P1001  
 P1002  
 P1003  
 P1004  
 P1005  
 P1006  
 P1007  
 P1008  
 P1009  
 P1010  
 P1011  
 P1012  
 P1013  
 P1014  
 P1015  
 P1016  
 P1017  
 P1018  
 P1019  
 P1020  
 P1021  
 P1022  
 P1023  
 P1024  
 P1025  
 P1026  
 P1027  
 P1028  
 P1029  
 P1030  
 P1031  
 P1032  
 P1033  
 P1034  
 P1035  
 P1036  
 P1037  
 P1038  
 P1039  
 P1040  
 P1041  
 P1042  
 P1043  
 P1044  
 P1045  
 P1046  
 P1047  
 P1048  
 P1049  
 P1050  
 P1051  
 P1052  
 P1053  
 P1054  
 P1055  
 P1056  
 P1057  
 P1058  
 P1059  
 P1060  
 P1061  
 P1062  
 P1063  
 P1064  
 P1065  
 P1066  
 P1067  
 P1068  
 P1069  
 P1070  
 P1071  
 P1072  
 P1073  
 P1074  
 P1075  
 P1076  
 P1077  
 P1078  
 P1079  
 P1080  
 P1081  
 P1082  
 P1083  
 P1084  
 P1085  
 P1086  
 P1087  
 P1088  
 P1089  
 P1090  
 P1091  
 P1092  
 P1093  
 P1094  
 P1095  
 P1096  
 P1097  
 P1098  
 P1099  
 P1100  
 P1101  
 P1102  
 P1103  
 P1104  
 P1105  
 P1106  
 P1107  
 P1108  
 P1109  
 P1110  
 P1111  
 P1112  
 P1113  
 P1114  
 P1115  
 P1116  
 P1117  
 P1118  
 P1119  
 P1120  
 P1121  
 P1122  
 P1123  
 P1124  
 P1125  
 P1126  
 P1127  
 P1128  
 P1129  
 P1130  
 P1131  
 P1132  
 P1133  
 P1134  
 P1135  
 P1136  
 P1137  
 P1138  
 P1139  
 P1140  
 P1141  
 P1142  
 P1143  
 P1144  
 P1145  
 P1146  
 P1147  
 P1148  
 P1149  
 P1150  
 P1151  
 P1152  
 P1153  
 P1154  
 P1155  
 P1156  
 P1157  
 P1158  
 P1159  
 P1160  
 P1161  
 P1162  
 P1163  
 P1164  
 P1165  
 P1166  
 P1167  
 P1168  
 P1169  
 P1170  
 P1171  
 P1172  
 P1173  
 P1174  
 P1175  
 P1176  
 P1177  
 P1178  
 P1179  
 P1180  
 P1181  
 P1182  
 P1183  
 P1184  
 P1185  
 P1186  
 P1187  
 P1188  
 P1189  
 P1190  
 P1191  
 P1192  
 P1193  
 P1194  
 P1195  
 P1196  
 P1197  
 P1198  
 P1199  
 P1200  
 P1201  
 P1202  
 P1203  
 P1204  
 P1205  
 P1206  
 P1207  
 P1208  
 P1209  
 P1210  
 P1211  
 P1212  
 P1213  
 P1214  
 P1215  
 P1216  
 P1217  
 P1218  
 P1219  
 P1220  
 P1221  
 P1222  
 P1223  
 P1224  
 P1225  
 P1226  
 P1227  
 P1228  
 P1229  
 P1230  
 P1231  
 P1232  
 P1233  
 P1234  
 P1235  
 P1236  
 P1237  
 P1238  
 P1239  
 P1240  
 P1241  
 P1242  
 P1243  
 P1244  
 P1245  
 P1246  
 P1247  
 P1248  
 P1249  
 P1250  
 P1251  
 P1252  
 P1253  
 P1254  
 P1255  
 P1256  
 P1257  
 P1258  
 P1259  
 P1260  
 P1261  
 P1262  
 P1263  
 P1264  
 P1265  
 P1266  
 P1267  
 P1268  
 P1269  
 P1270  
 P1271  
 P1272  
 P1273  
 P1274  
 P1275  
 P1276  
 P1277  
 P1278  
 P1279  
 P1280  
 P1281  
 P1282  
 P1283  
 P1284  
 P1285  
 P1286  
 P1287  
 P1288  
 P1289  
 P1290  
 P1291  
 P1292  
 P1293  
 P1294  
 P1295  
 P1296  
 P1297  
 P1298  
 P1299  
 P1300  
 P1301  
 P1302  
 P1303  
 P1304  
 P1305  
 P1306  
 P1307  
 P1308  
 P1309  
 P1310  
 P1311  
 P1312  
 P1313  
 P1314  
 P1315  
 P1316  
 P1317  
 P1318  
 P1319  
 P1320  
 P1321  
 P1322  
 P1323  
 P1324  
 P1325  
 P1326  
 P1327  
 P1328  
 P1329  
 P1330  
 P1331  
 P1332  
 P1333  
 P1334  
 P1335  
 P1336  
 P1337  
 P1338  
 P1339  
 P1340  
 P1341  
 P1342  
 P1343  
 P1344  
 P1345  
 P1346  
 P1347  
 P1348  
 P1349  
 P1350  
 P1351  
 P1352  
 P1353  
 P1354  
 P1355  
 P1356  
 P1357  
 P1358  
 P1359  
 P1360  
 P1361  
 P1362  
 P1363  
 P1364  
 P1365  
 P1366  
 P1367  
 P1368  
 P1369  
 P1370  
 P1371  
 P1372  
 P1373  
 P1374  
 P1375  
 P1376  
 P1377  
 P1378  
 P1379  
 P1380  
 P1381  
 P1382  
 P1383  
 P1384  
 P1385  
 P1386  
 P1387  
 P1388  
 P1389  
 P1390  
 P1391  
 P1392  
 P1393  
 P1394  
 P1395  
 P1396  
 P1397  
 P1398  
 P1399  
 P1400  
 P1401  
 P1402  
 P1403  
 P1404  
 P1405  
 P1406  
 P1407  
 P1408  
 P1409  
 P1410  
 P1411  
 P1412  
 P1413  
 P1414  
 P1415  
 P1416  
 P1417  
 P1418  
 P1419  
 P1420  
 P1421  
 P1422  
 P1423  
 P1424  
 P1425  
 P1426  
 P1427  
 P1428  
 P1429  
 P1430  
 P1431  
 P1432  
 P1433  
 P1434  
 P1435  
 P1436  
 P1437  
 P1438  
 P1439  
 P1440  
 P1441  
 P1442  
 P1443  
 P1444  
 P1445  
 P1446  
 P1447  
 P1448  
 P1449  
 P1450  
 P1451  
 P1452  
 P1453  
 P1454  
 P1



CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the  
 CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1  
 CC (resp.) (see AAN30156, AAN30223). In the examples plasmids pCMV5 and  
 CC pCMV10/IF2-beta-1 and F alpha-4A were used (see AAN30151, AAN30152,  
 CC AAN30157). HindIII was used to digest the DNA sequences in the region  
 CC of significant homologies (see AAN30153, AAN30154, AAN30158, AAN30159).  
 CC and the restriction fragments were ligated to form hybrid DNA.  
 CC  
 XX  
 SO Sequence 166 AA:  
 alignment\_scores:  
 Quality: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273  
 alignment\_block:  
 US-09-832-658-7 x AAP30219 ..  
 seq\_name: /1 to: AAP30219 from: 1 to: 166  
 seq\_documentation\_block:  
 ID AAP50024 standard: Protein: 166 AA.  
 AC AAP50024:  
 XX  
 XX 04-SEP-1991 (first entry)  
 XX  
 XX Sequence of new modified human beta interferon polypeptides  
 CC IFN-41B.  
 CC  
 CC Antiviral; cell growth regulator; immune system regulator;  
 CC antiproliferative.  
 CC  
 CC Homo sapiens.  
 CC  
 CC EP163993-A.  
 CC  
 CC 11-DEC-1985.  
 CC  
 CC 17-MAY-1985: 85EP-0105750.  
 CC  
 CC 17-MAY-1984: 84GB-0012564.  
 CC  
 CC (SEAR) SEARLE G D & CO.  
 CC  
 CC Bell ID, Roseley PG, Porter AG:  
 CC  
 CC WPI: 1985-411944/50.  
 CC N-PSDB: AAN50025.  
 CC  
 CC New modified human beta interferon polypeptide(s) - prepd. by  
 CC plasmid transformed bacteria, with improved antiviral,  
 CC antiproliferative and immune regulating actions  
 CC  
 CC Claim 16: Chart 2c, page 3d, 71pp: English.  
 CC  
 CC  
 CC Compared with interferon beta prepd. by recombinant methods, the  
 CC INPs of the invention are more active and have different affinities  
 CC for cell surface receptors (allowing selective targeting); they  
 CC have higher therapeutic index; improved stability against microbial  
 CC breakdown during synthesis; and better in vivo solubility and  
 CC stability. They are also easier to recover from incubation mixts.

XX  
 SO Sequence 166 AA:  
 alignment\_scores:  
 Quality: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273  
 alignment\_block:  
 US-09-832-658-7 x AAP50024 ..  
 Align seq 1/1 to: AAP50024 from: 1 to: 166  
 seq\_documentation\_block:  
 ID AAP50026 standard: Protein: 166 AA.  
 AC AAP50026:  
 XX  
 XX 04-SEP-1991 (first entry)  
 XX  
 XX Sequence of new modified human beta interferon polypeptides  
 CC IFN-44A.  
 CC  
 CC Antiviral; cell growth regulator; immune system regulator;  
 CC antiproliferative.  
 CC  
 CC Homo sapiens.  
 CC  
 CC EP163993-A.  
 CC  
 CC 11-DEC-1985.  
 CC  
 CC 17-MAY-1985: 85EP-0105750.  
 CC  
 CC 17-MAY-1984: 84GB-0012564.  
 CC  
 CC (SEAR) SEARLE G D & CO.  
 CC  
 CC Bell ID, Roseley PG, Porter AG:  
 CC  
 CC WPI: 1985-311944/50.  
 CC N-PSDB: AAN50027.  
 CC  
 CC New modified human beta interferon polypeptide(s) - prepd. by  
 CC plasmid transformed bacteria, with improved antiviral,  
 CC antiproliferative and immune regulating actions  
 CC  
 CC Claim 18: Chart 2e, page 3e: 71pp: English.  
 CC  
 CC  
 CC Compared with interferon beta prepd. by recombinant methods, the  
 CC INPs of the invention are more active and have different affinities  
 CC for cell surface receptors (allowing selective targeting); they  
 CC have higher therapeutic index; improved stability against microbial  
 CC breakdown during synthesis; and better in vivo solubility and  
 CC stability. They are also easier to recover from incubation mixts.

alignment\_scores:  
 Quality: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0

















Smith, L., Patel, L.D., Lewis, H.M., Porter, A.G., Birch, J.R.,  
 Guteridge, L., Carey, N.H.,  
 "The amino terminal sequence of human fibroblast interferon as  
 deduced from reverse transcripts obtained using synthetic  
 oligonucleotide primers,"  
 Nucleic Acids Res. 18(13): 4941(1990).  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525  
 526  
 527  
 528  
 529  
 530  
 531  
 532  
 533  
 534  
 535  
 536  
 537  
 538  
 539  
 540  
 541  
 542  
 543  
 544  
 545  
 546  
 547  
 548  
 549  
 550  
 551  
 552  
 553  
 554  
 555  
 556  
 557  
 558  
 559  
 560  
 561  
 562  
 563  
 564  
 565  
 566  
 567  
 568  
 569  
 570  
 571  
 572  
 573  
 574  
 575  
 576  
 577  
 578  
 579  
 580  
 581  
 582  
 583  
 584  
 585  
 586  
 587  
 588  
 589  
 590  
 591  
 592  
 593  
 594  
 595  
 596  
 597  
 598  
 599  
 600  
 601  
 602  
 603  
 604  
 605  
 606  
 607  
 608  
 609  
 610  
 611  
 612  
 613  
 614  
 615  
 616  
 617  
 618  
 619  
 620  
 621  
 622  
 623  
 624  
 625  
 626  
 627  
 628  
 629  
 630  
 631  
 632  
 633  
 634  
 635  
 636  
 637  
 638  
 639  
 640  
 641  
 642  
 643  
 644  
 645  
 646  
 647  
 648  
 649  
 650  
 651  
 652  
 653  
 654  
 655  
 656  
 657  
 658  
 659  
 660  
 661  
 662  
 663  
 664  
 665  
 666  
 667  
 668  
 669  
 670  
 671  
 672  
 673  
 674  
 675  
 676  
 677  
 678  
 679  
 680  
 681  
 682  
 683  
 684  
 685  
 686  
 687  
 688  
 689  
 690  
 691  
 692  
 693  
 694  
 695  
 696  
 697  
 698  
 699  
 700  
 701  
 702  
 703  
 704  
 705  
 706  
 707  
 708  
 709  
 710  
 711  
 712  
 713  
 714  
 715  
 716  
 717  
 718  
 719  
 720  
 721  
 722  
 723  
 724  
 725  
 726  
 727  
 728  
 729  
 730  
 731  
 732  
 733  
 734  
 735  
 736  
 737  
 738  
 739  
 740  
 741  
 742  
 743  
 744  
 745  
 746  
 747  
 748  
 749  
 750  
 751  
 752  
 753  
 754  
 755  
 756  
 757  
 758  
 759  
 760  
 761  
 762  
 763  
 764  
 765  
 766  
 767  
 768  
 769  
 770  
 771  
 772  
 773  
 774  
 775  
 776  
 777  
 778  
 779  
 780  
 781  
 782  
 783  
 784  
 785  
 786  
 787  
 788  
 789  
 790  
 791  
 792  
 793  
 794  
 795  
 796  
 797  
 798  
 799  
 800  
 801  
 802  
 803  
 804  
 805  
 806  
 807  
 808  
 809  
 810  
 811  
 812  
 813  
 814  
 815  
 816  
 817  
 818  
 819  
 820  
 821  
 822  
 823  
 824  
 825  
 826  
 827  
 828  
 829  
 830  
 831  
 832  
 833  
 834  
 835  
 836  
 837  
 838  
 839  
 840  
 841  
 842  
 843  
 844  
 845  
 846  
 847  
 848  
 849  
 850  
 851  
 852  
 853  
 854  
 855  
 856  
 857  
 858  
 859  
 860  
 861  
 862  
 863  
 864  
 865  
 866  
 867  
 868  
 869  
 870  
 871  
 872  
 873  
 874  
 875  
 876  
 877  
 878  
 879  
 880  
 881  
 882  
 883  
 884  
 885  
 886  
 887  
 888  
 889  
 890  
 891  
 892  
 893  
 894  
 895  
 896  
 897  
 898  
 899  
 900  
 901  
 902  
 903  
 904  
 905  
 906  
 907  
 908  
 909  
 910  
 911  
 912  
 913  
 914  
 915  
 916  
 917  
 918  
 919  
 920  
 921  
 922  
 923  
 924  
 925  
 926  
 927  
 928  
 929  
 930  
 931  
 932  
 933  
 934  
 935  
 936  
 937  
 938  
 939  
 940  
 941  
 942  
 943  
 944  
 945  
 946  
 947  
 948  
 949  
 950  
 951  
 952  
 953  
 954  
 955  
 956  
 957  
 958  
 959  
 960  
 961  
 962  
 963  
 964  
 965  
 966  
 967  
 968  
 969  
 970  
 971  
 972  
 973  
 974  
 975  
 976  
 977  
 978  
 979  
 980  
 981  
 982  
 983  
 984  
 985  
 986  
 987  
 988  
 989  
 990  
 991  
 992  
 993  
 994  
 995  
 996  
 997  
 998  
 999  
 1000

alignment\_scores:  
 Quality: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

alignment\_block:  
 US-09-832-658-7 X INB\_HUMAN  
 Align seq 1/1 to: INB\_HUMAN from: 1 to: 187

21 ATGCTTACGCGCTCTTCTGAGCGCTGAACTTTGATGATGAGTGG  
 TTTCTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT  
 22 MetSerCysPheMetCysCysPheMetCysCysSerAspMetCys  
 71 TCGAAGCTCTCTGCG 86  
 TTTT TTTT TTTT TTTT  
 38 SerMetGluMetCysPhe 43

seq\_name: SwissProt\_40:DREB\_HUMAN

seq\_documentation\_block:  
 ID DREB\_HUMAN STANDARD; PRI: 649 AA.  
 AC Q16643;  
 DT 01-NOV-1997 (Rel. 45, created)  
 DT 01-NOV-1997 (Rel. 45, last sequence update)  
 DE 15-0007-2001 (Rel. 40, last annotation update)  
 DE Dreb1b p.  
 GN DBN1.  
 OS Homo sapiens (Human).  
 PE Eukaryotic Metazoa; Chordata; Vertebrata; Euteleostomi;  
 PE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID 9606;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: osteoblast;  
 RA FISHER L.W., MURPHY G.W., FILIPULA D., IZAKI K., YOUNG M.L.;  
 KT "Human dreb1b cDNA sequence, mRNA tissue distribution and  
 KT chromosomal localization";  
 RT Neurosci. Res. Commun. 14:45-47(1994).  
 RN 121  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: fetal brain;  
 RA MEDLINE:94030846; PubMed 8216429;  
 SA "dreb1b cDNA sequence, mRNA tissue distribution and  
 RT mapping of its gene";  
 RT Molecular cloning of cDNA encoding human dreb1b and chromosomal  
 RT mapping of its gene";  
 RT Biochem. Biophys. Res. Commun. 196:468-472(1994).  
 RN 131  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: Eye;  
 RA STRAUSSER R.;  
 RC Subcloned (Nov 2000) to the new genome/DBM databases.  
 CC 1- FUNCTION: DREBRINS MIGHT PLAY SOME ROLE IN CELL MIGRATION,  
 CC EXTENSION OF NEURONAL PROCESSES AND PLASTICITY OF DENDRITES.  
 CC RESPECTIVELY, BINDS ACTIN.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC 1- TISSUE SPECIFICITY: BRAIN NEURONS, ALSO FOUND IN THE HEART,  
 CC PLACENTA, SKELETAL MUSCLE, KIDNEY AND PANCREAS.

-----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation.  
 The European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed, altered by and for commercial  
 activities or used in any way to promote a product or service.  
 or send an email to [liscons@isb-sib.ch](mailto:liscons@isb-sib.ch).

EMBL: 000802; AA016256.1;  
 EMBL: 017540; AA04480.1;  
 EMBL: BC000284; AA00284.1;  
 MIM: 126607;  
 DR InterPro: IPR002108; Col1in\_ADF;  
 DR Pfam: PF00241; Col1in\_ADF; 1.

EMBL: SM00102; ADF: 1.  
 Acc to Bioinformatics: Brain; Neuronal.  
 SOURCE: 649 AA; 71425 MW; A17205255C22098 CR664.

alignment\_scores:  
 Quality: 49.50 Length: 29  
 Ratio: 2.152 Gaps: 1  
 Percent Similarity: 79.310 Percent Identity: 41.379

alignment\_block:

US-09-832-658-7 x DREF\_HUMAN

Align seq 1/1 to: DREF\_HUMAN from: 1 to: 649

3 GGAGACGATGATGACAGACAGATGCTTACGCTCTGAGAGCTAA.. 50  
 |||||  
 47 GlySerAspAspLeuLysLeuAlaLaserGlyGlyGlyLeuGlnG1 53  
 51 .GCTTCTAGCAATTTTCAGTGTGACAGAGCTCTCTGG 86  
 |||||  
 53 uduSerGlyHisPheGlnAsnGlnLysValMetTyr 65

seq\_name: SwissProt\_40:DREF\_RAT

seq\_documentation\_block:

ID: DREF\_RAT STANDARD: PRT: 707 AA.

AC: 007266;

DT: 01-NOV-1997 (Rel. 35, Created)

DI: 01-NOV-1997 (Rel. 35, Last sequence update)

DE: 01-NOV-1997 (Rel. 35, Last annotation update)

FE: Drefrin A.

GN: Drefrin A.

OS: Rattus norvegicus (Rat).

OC: Mammalia; Metazoa; Chordata; Vertebrata; Eucaryota;

OF: Mammalia; Eutheria; Rodentia; Sciurinae; Muridae; Rattus.

OX: NBT\_LaXid-10116.

RN: 111

RP: SOURCE FROM N.A.

RC: STRAIN Wistar; Tissue: Brain; and Hippocampus;

EX: Medium: 9285233; PubMed: 161026;

KA: Shitka T., Ohada N., Chata K.;

RT: "Cloning of drefrin A and induction of neurite-like processes in

RT: drefrin-transfected cells."

CC: -1- FUNCTION: DREFRIN MIGHT PLAY SOME ROLE IN CELL MIGRATION.

CC: -1- EXTENSION OF NEURONAL PROCESSES AND PLASTICITY OF DENDRITES,

CC: RESPECTIVELY, BINDS ACTIN.

CC: -1- SUBCELLULAR LOCATION: Cytoplasmic

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

CC: -1- ALTERNATIVE PRODUCTS. REGULATE FORMS OF DREFRIN EXPERT FROM

alignment\_scores:  
 Quality: 49.50 Length: 29  
 Ratio: 2.152 Gaps: 1  
 Percent Similarity: 79.310 Percent Identity: 41.379

alignment\_block:

US-09-832-658-7 x DREF\_RAT

Align seq 1/1 to: DREF\_RAT from: 1 to: 707

3 GGAGACGATGATGACAGACAGATGCTTACGCTCTGAGAGCTAA.. 50  
 |||||  
 47 GlySerAspAspLeuLysLeuAlaLaserGlyGlyGlyLeuGlnG1 53  
 51 .GCTTCTAGCAATTTTCAGTGTGACAGAGCTCTCTGG 86  
 |||||  
 53 uduSerGlyHisPheGlnAsnGlnLysValMetTyr 65

seq\_name: SwissProt\_40:PTPR\_CHLTR

seq\_documentation\_block:

ID: PTPR\_CHLTR STANDARD: PRT: 109 AA.

AC: 084341;

DT: 16-OCT-2001 (Rel. 40, Created)

DI: 16-OCT-2001 (Rel. 40, Last sequence update)

DE: 16-OCT-2001 (Rel. 40, Last annotation update)

DE: Phosphotransfer protein PTP (Histidine-containing protein).

GN: PTPH OR CT337.

OS: Chlamydia trachomatis.

OC: Bacteria; Chlamydiales; Chlamydiae; Chlamydia.

OX: NCBI\_Taxid-813;

RN: 111

RP: SEQUENCE FROM N.A.

RC: STRAIN D/1W-3/CX;

EX: Medline: 9900809; PubMed: 9784136;

KA: Stephens R.S., Kaiman S., Lammell C.D., Fan J., Marathe R., Aravind L.,

KA: Mitchell W.E., Glinger L., Talusov R.L., Zhao Y., Koonin E.V.,

KA: Davis R.W.;

RT: "Genome sequence of an obligate intracellular pathogen of humans:

RT: Chlamydia trachomatis."

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE

CC: -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOTRANSFER SYSTEM (PTP). A MAJOR CARBOHYDRATE











- RA MEDLINE 96154723; PubMed 9596678;  
RA SAVITSKY K., Stev S., Tadio D.A., Ziv Y., Sartiel A., Collins F.S.,  
RA Shiloh Y., Rotman G.,  
RA "The complete sequence of the coding region of the ATM gene reveals  
RA similarity to cell cycle regulators in different species."  
RA Hum. Mol. Genet. 4:2025-2032(1995).  
RA [10]
- RA SEQUENCE FROM N.A.  
RA MEDLINE 97343427; PubMed 9199932;  
RA Plattner M., Rotman G., Rance D., Ozick T., Savitsky K., Bar-Shira A.,  
RA Gilad S., Shiloh Y., Rosenthal A.,  
RA "Ataxia-telangiectasia locus: sequence analysis of 184 kb of human  
RA genomic DNA containing the entire ATM gene."  
RA Genom. Res. 7:592-605(1997).  
RA [11]
- RA SEQUENCE OF 1-24 FROM N.A.  
RA MEDLINE 97267790; PubMed 9108147;  
RA SAVITSKY K., Eliezer M., Uziel T., Gilad S., Sartiel A., Rosenthal A.,  
RA Elroy-Stein O., Shiloh Y., Rotman G.,  
RA "Ataxia-telangiectasia: structural diversity of untranslated sequences  
RA suggests complex post transcriptional regulation of ATM gene  
RA expression."  
RA Nucleic Acids Res. 25:1678-1684(1997).  
RA [12]
- RA SEQUENCE OF 1-169 FROM N.A., AND VARIANT AT 2546-SEP-11F-2548 DEL.  
RA MEDLINE 96381449; PubMed 8789452;  
RA Hyatt P.J., McConville C.H., Cooper P., Parkhill J., Stanekovic T.,  
RA McDermott G.M., Thirk J.A., Taylor A.M.R.,  
RA "Mutations revealed by sequencing two 5' half of the gene for ataxia  
RA telangiectasia."  
RA Hum. Mol. Genet. 5:145-149(1996).  
RA [13]
- RA SEQUENCE OF 1449-3856 FROM N.A., AND VARIANT ASN-3003.  
RA MEDLINE 96105020; PubMed 8521992;  
RA Rasio D., Neufeld M., Croce C.M.,  
RA "Genomic organization of the ATM locus involved in ataxia-  
RA telangiectasia."  
RA Cancer Res. 55:6053-6057(1995).  
RA [14]
- RA SEQUENCE OF 1449-3056 FROM N.A., AND VARIANTS AT 2427-LEU-AMT-2428  
RA DEL; 2546-SEP-11F-2548 DEL AND SEP-2860 DEL.  
RA MEDLINE 95312868; PubMed 7792600;  
RA TISSOT-FIBROBLAST; PubMed 7792600;  
RA SAVITSKY K., Bar-Shira A., Gilad S., Rotman G., Ziv Y., Vanagaite L.,  
RA Tadio D.A., Smith S., Uziel T., Stev S., Ashkenazi M., Becker I.,  
RA Frydman M., Harnik R., Faltanali S.P., Simmons A., Cline G.A.,  
RA Sartiel A., Gatti R.A., Chessa L., Sanal O., Lavie M.F.,  
RA Jaspers N.G.J., Taylor A.M.R., Arlett C.F., Miki T., Weissman S.M.,  
RA Lovett M., Collins F.S., Shiloh Y.,  
RA "A single ataxia telangiectasia gene with a product similar to p1-3  
RA kinase."  
RA Science 268:1744-1748(1995).  
RA [15]
- RA PAIRED SEQUENCE FROM N.A., AND VARIANTS CYS-49, ARG-1054, PHE-1420;  
RA ILE-2079 AND ALA-2287.  
RA MEDLINE 96275238; PubMed 8665503;  
RA Vorobeyevsky I., Bastio P., Liu L., Monaco C., Hammarstrom L.,  
RA Wostear A.D.H., Eshkolik J., Bartholomew C., James M.R.,  
RA Russo G., Croce C.M., Neufeld M.,  
RA "The ATM gene and susceptibility to breast cancer: analysis of 38  
RA breast tumors reveals no evidence for mutation."  
RA Cancer Res. 56:2726-2732(1996).  
RA [16]
- RA PHOSPHORYLATION.  
RA MEDLINE 97126018; PubMed 8969240;  
RA Chen G., Lee E.Y.-H.P.,  
RA "The product of the ATM gene is a 370-kDa nuclear phosphoprotein."  
RA J. Biol. Chem. 271:34693-34697(1996).  
RA [17]
- RA SUBCELLULAR LOCATION.  
RA MEDLINE 97203148; PubMed 9050066;  
RA Brown K.D., Ziv Y., Sadanandan S.N., Chessa L., Collins F.S.,  
RA Shiloh Y., Tadio D.A.,  
RA "The ataxia-telangiectasia gene product, a constitutively expressed  
RA nuclear protein that is not up-regulated following genomic damage."  
RA Proc. Natl. Acad. Sci. U.S.A. 94:1840-1845(1997).  
RA [18]
- RA SUBCELLULAR LOCATION AND VARIANTS AT 2946 S 1-2548 DEL ARE Y 2924.  
RA MEDLINE 97294602; PubMed 9150358;  
RA Walters D., Khanna K.K., Beamish H., Bittori G., Spring K., Kuhl P.,  
RA Walters D., Khanna K.K., Khanna K., Kozlov S., Zhang N., Farrell A.,  
RA Gatti R.A., Gatti R.A., Lavie M.F.,  
RA Ramsay J., Gatti R.A., Lavie M.F.,  
RA "Cellular localization of the ataxia-telangiectasia (ATM) gene product  
RA and distribution between mutated and normal forms."  
RA Oncogene 14:1911-1921(1997).  
RA [19]
- RA KINASE ACTIVITY.  
RA MEDLINE 97141775; PubMed 8988033;  
RA Jung M., Kondratyev A., Lee S.A.,  
RA "ATM gene product phosphorylates 1 kappa B-alpha."  
RA Cancer Res. 57:24-27(1997).  
RA [20]
- RA C-ABL BINDING.  
RA MEDLINE 97311400; PubMed 9168117;  
RA Shafran T., Khanna K.K., Kedar P., Spring K., Yen T.,  
RA Hobson K., Gatti M., Zhang N., Walters D., Barton M., Shiloh Y.,  
RA Khanna K.K., Kufe D., Lavie M.F.,  
RA "Interaction between ATM protein and c-Abl in response to DNA  
RA damage."  
RA Nature 387:520-523(1997).  
RA [21]
- RA P53 BINDING AND KINASE ACTIVITY.  
RA MEDLINE 96967451; PubMed 9644217;  
RA Khanna K.K., Kozlov S., Scott S., Gatti M., Khanna K.,  
RA Khanna K.K., Kozlov S., Chan D., Lee-Miller S.P., Lavie M.F.,  
RA "ATM associates with and phosphorylates p53: mapping the region of  
RA interaction."  
RA Nat. Genet. 20:398-400(1998).  
RA [22]
- RA p14-AVAPRIN BINDING.  
RA MEDLINE 98373420; PubMed 9707615;  
RA Lim D.-S., Kirsch D.G., Camman C.F., Ahn J.-H., Ziv Y., Newman L.S.,  
RA Darnell R.B., Shiloh Y., Kastan M.B.,  
RA "ATM binds to beta adaphin in cytoplasmic vesicles."  
RA Proc. Natl. Acad. Sci. U.S.A. 95:10146-10151(1998).  
RA [23]
- RA PHOSPHORYLATION OF P53.  
RA MEDLINE 9649473; PubMed 9733514;  
RA Rabin S., Moyal L., Shieh S.-Y., Taya Y., Anderson C.W., Chessa L.,  
RA Shmuelinsky N., Prives C., Peles Y., Shiloh Y., Ziv Y.,  
RA "enhanced phosphorylation of p53 by ATM in response to DNA damage."  
RA Science 281:1674-1677(1998).  
RA [24]
- RA PHOSPHORYLATION OF P53, AND MUTAGENESIS OF ASP-2870 AND ASN-2875.  
RA MEDLINE 98404274; PubMed 9733515;  
RA Camman C.E., Lim D.-S., Complich R.A., Taya Y., Janai K.,  
RA Sakaguchi K., Appella E., Kastan M.B., Sliceman J.D.,  
RA "Activation of the ATM kinase by ionizing radiation and  
RA phosphorylation of p53."  
RA Science 281:1677-1679(1998).  
RA [25]
- RA DNA BINDING.  
RA MEDLINE 99432198; PubMed 10500142;  
RA Smith G.C.H., Gary P.B., Lakin N.D., Hann B.C., Teo S.H., Chen D.,  
RA Jacobson S.P.,  
RA "Purification and DNA binding properties of the ataxia telangiectasia  
RA gene product ATM."  
RA Proc. Natl. Acad. Sci. U.S.A. 96:11134-11139(1999).  
RA [26]
- RA PHOSPHORYLATION OF BRCA1.  
RA MEDLINE 972018333; PubMed 10550055;  
RA Corbett D., Wang Y., Qin J., Elledge S.J.,  
RA "Requirement of ATM-dependent phosphorylation of brca1 in the DNA  
RA damage response to double-strand breaks."  
RA Science 285:1162-1166(1999).  
RA [27]























$$: \text{SiO} \quad 10 \quad \text{N} \quad 7$$

alignment\_scores:

```
alignment_scores: 89.00
quality:
length: 22
```

Patent: 4,944      Class: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

US-09-832-658-7 x US-09-832-658-7

Align seq 1/1    to: US-09-832-658-7    from: 1    to: 166

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

COMPUTER READABLE FORM:

1 MEDICAL TYPE: floppy disk

2 COMPUTER: IBM PC compatible

3 OPERATING SYSTEM: PC-DOS/MS-DOS

4 SOFTWARE: PatentIn Release #1.0, Version #1.25

5 CURRENT APPLICATION DATA:

6 APPLICATION NUMBER: US-09-832-658-7

7 FILING DATE: 1993-03-05

8 CLASSIFICATION: 424

9 ATTORNEY/AGENT INFORMATION:

10 NAME: Oblin, No. 5780021man P.

11 REGISTRATION NUMBER: 24,618

12 REFERENCE/DOCKET NUMBER: 1126, 096, 0

13 TELECOMMUNICATION INFORMATION:

14 TELEPHONE: (703) 413-4000

15 TELEFAX: (703) 413-2220

16 FAX: 248855 OPAT DR

17 INFORMATION FOR SEQ ID NO: 22:

18 SEQUENCE CHARACTERISTICS:

19 LENGTH: 187 amino acids

20 TYPE: amino acid

21 TOPOLOGY: unknown

22 MOLECULE TYPE: protein

23 FEATURE:

24 NAME/KEY: Protein

25 LOCATION: 22-187

26 OTHER INFORMATION: /note "Hb-1FN-beta"

US-08-026-758-22

Alignment scores:

Quality: 89.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

Align seq 1/1    to: US-08-026-758-22    from: 1    to: 187

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273

seq document\_block:

1 Alignment scores: 100.00      Length: 22  
 Ratio: 4.544      Gaps: 0  
 Percent Similarity: 81.818      Percent Identity: 77.273



alignment scores:

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment block:  
 US-09-832-658-7 x US-09-206-936-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

alignment scores:

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment block:  
 US-09-832-658-7 x US-09-206-936-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

alignment scores:

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment block:  
 US-09-832-658-7 x US-09-206-936-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

CURRENT APPLICATION NUMBER: US-09-206-935-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment block:  
 US-09-206-935-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment block:  
 US-09-206-935-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

alignment scores:

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment block:  
 US-09-206-935-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment block:  
 US-09-832-658-7 x US-09-206-936-7

21 Alignment scores: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

SQL\_documentation\_block:

1 Patent No. 5426859  
 2 APPLICANT: SUGANO, HARUO;MURAMATSU, MASAMI;TANIGUCHI, TADATSUGU  
 3 TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID  
 4 NUMBER OF SEQUENCES: 3  
 5 CURRENT APPLICATION DATA:  
 6 APPLICATION NUMBER: 05/06/201, 459  
 7 FILING DATE: 27-OCT-1980  
 8 SEQ ID NO:1:  
 9 LENGTH:187  
 10 5426859-1

alignment scores:

Quality: 89.00 Length: 22  
 Ratio: 4.944 Gaps: 0  
 Percent Similarity: 81.818 Percent Identity: 77.273

Alignment\_block:  
 19 842 658 7 x 5426859-1 ..

Align seq 1/1 to: 5426859-1 from: 1 to: 187

21 ATGAGTTACAGCCATCTTACAGCCCTACAAAGTTCTAGTAATTTCAGTG 70  
 22 MetSerTyrAsnLeuLeuGlyPheLeuGluIleArgSerTAspHeGlnCys 38  
 71 TTTAAAGTTCTGTGG 86  
 78 sGlnTysLeuLeuIleTrp 43

